



Corrected sequence listing 11-07  
SEQUENCE LISTING

<110> Consortium fuer elektrochemische Industrie GmbH

<120> Feedback-resistant Homoserine-Transsuccinylases

<130> CO-P#####

<140> 10530843

<141> 2007-11-14

<160> 12

<170> PatentIn Ver. 2.0

<210> 1

<211> 930

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)..(930)

<300>

<301> Blattner, F. R.

<302> The complete genome sequence of Escherichia coli K-12.

<303> Science

<304> 277

<305> 5331

<306> 1453-1474

<307> 1997

<400> 1

atg ccg att cgt gtg ccg gac gag cta ccc gcc gtc aat ttc ttg cgt	48
Met Pro Ile Arg Val Pro Asp Glu Leu Pro Ala Val Asn Phe Leu Arg	
1 5 10 15	

gaa gaa aac gtc ttt gtg atg aca act tct cgt gcg tct ggt cag gaa	96
Glu Glu Asn Val Phe Val Met Thr Thr Ser Arg Ala Ser Gly Gln Glu	
20 25 30	

att cgt cca ctt aag gtt ctg atc ctt aac ctg atg ccg aag aag att	144
Ile Arg Pro Leu Lys Val Leu Ile Leu Asn Leu Met Pro Lys Lys Ile	
35 40 45	

gaa act gaa aat cag ttt ctg cgc ctg ctt tca aac tca cct ttg cag	192
Glu Thr Glu Asn Gln Phe Leu Arg Leu Leu Ser Asn Ser Pro Leu Gln	
50 55 60	

gtc gat att cag ctg ttg cgc atc gat tcc cgt gaa tcg cgc aac acg	240
Val Asp Ile Gln Leu Leu Arg Ile Asp Ser Arg Glu Ser Arg Asn Thr	
65 70 75 80	

ccc gca gag cat ctg aac aac ttc tac tgt aac ttt gaa gat att cag	288
Pro Ala Glu His Leu Asn Asn Phe Tyr Cys Asn Phe Glu Asp Ile Gln	
85 90 95	

gat cag aac ttt gac ggt ttg att gta act ggt gcg ccg ctg ggc ctg	336
Asp Gln Asn Phe Asp Gly Leu Ile Val Thr Gly Ala Pro Leu Gly Leu	
100 105 110	

Corrected sequence listing 11-07

gtg gag ttt aat gat gtc gct tac tgg ccg cag atc aaa cag gtg ctg	384
Val Glu Phe Asn Asp Val Ala Tyr Trp Pro Gln Ile Lys Gln Val Leu	
115 120 125	
gag tgg tcg aaa gat cac gtc acc tcg acg ctg ttt gtc tgc tgg gcg	432
Glu Trp Ser Lys Asp His Val Thr Ser Thr Leu Phe Val Cys Trp Ala	
130 135 140	
gta cag gcc gcg ctc aat atc ctc tac ggc att cct aag caa act cgc	480
Val Gln Ala Ala Leu Asn Ile Leu Tyr Gly Ile Pro Lys Gln Thr Arg	
145 150 155 160	
acc gaa aaa ctc tct ggc gtt tac gag cat cat att ctc cat cct cat	528
Thr Glu Lys Leu Ser Gly Val Tyr Glu His His Ile Leu His Pro His	
165 170 175	
gcg ctt ctg acg cgt ggc ttt gat gat tca ttc ctg gca ccg cat tcg	576
Ala Leu Leu Thr Arg Gly Phe Asp Asp Ser Phe Leu Ala Pro His Ser	
180 185 190	
cgc tat gct gac ttt ccg gca gcg ttg att cgt gat tac acc gat ctg	624
Arg Tyr Ala Asp Phe Pro Ala Ala Leu Ile Arg Asp Tyr Thr Asp Leu	
195 200 205	
gaa att ctg gca gag acg gaa gaa ggg gat gca tat ctg ttt gcc agt	672
Glu Ile Leu Ala Glu Thr Glu Glu Gly Asp Ala Tyr Leu Phe Ala Ser	
210 215 220	
aaa gat aag cgc att gcc ttt gtg acg ggc cat ccc gaa tat gat gcg	720
Lys Asp Lys Arg Ile Ala Phe Val Thr Gly His Pro Glu Tyr Asp Ala	
225 230 235 240	
caa acg ctg gcg cag gaa ttt ttc cgc gat gtg gaa gcc gga cta gac	768
Gln Thr Leu Ala Gln Glu Phe Phe Arg Asp Val Glu Ala Gly Leu Asp	
245 250 255	
ccg gat gta ccg tat aac tat ttc ccg cac aat gat ccg caa aat aca	816
Pro Asp Val Pro Tyr Asn Tyr Phe Pro His Asn Asp Pro Gln Asn Thr	
260 265 270	
ccg cga gcg agc tgg cgt agt cac ggt aat tta ctg ttt acc aac tgg	864
Pro Arg Ala Ser Trp Arg Ser His Gly Asn Leu Leu Phe Thr Asn Trp	
275 280 285	
ctc aac tat tac gtc tac cag atc acg cca tac gat cta cgg cac atg	912
Leu Asn Tyr Tyr Val Tyr Gln Ile Thr Pro Tyr Asp Leu Arg His Met	
290 295 300	
aat cca acg ctg gat taa	930
Asn Pro Thr Leu Asp	
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<210> 2  
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 <212> PRT  
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<400> 2  
 Met Pro Ile Arg Val Pro Asp Glu Leu Pro Ala Val Asn Phe Leu Arg  
 1 5 10 15

Corrected sequence listing 11-07

Glu Glu Asn Val Phe Val Met Thr Thr Ser Arg Ala Ser Gly Gln Glu  
20 25 30  
Ile Arg Pro Leu Lys Val Leu Ile Leu Asn Leu Met Pro Lys Lys Ile  
35 40 45  
Glu Thr Glu Asn Gln Phe Leu Arg Leu Leu Ser Asn Ser Pro Leu Gln  
50 55 60  
Val Asp Ile Gln Leu Leu Arg Ile Asp Ser Arg Glu Ser Arg Asn Thr  
65 70 75 80  
Pro Ala Glu His Leu Asn Asn Phe Tyr Cys Asn Phe Glu Asp Ile Gln  
85 90 95  
Asp Gln Asn Phe Asp Gly Leu Ile Val Thr Gly Ala Pro Leu Gly Leu  
100 105 110  
Val Glu Phe Asn Asp Val Ala Tyr Trp Pro Gln Ile Lys Gln Val Leu  
115 120 125  
Glu Trp Ser Lys Asp His Val Thr Ser Thr Leu Phe Val Cys Trp Ala  
130 135 140  
Val Gln Ala Ala Leu Asn Ile Leu Tyr Gly Ile Pro Lys Gln Thr Arg  
145 150 155 160  
Thr Glu Lys Leu Ser Gly Val Tyr Glu His His Ile Leu His Pro His  
165 170 175  
Ala Leu Leu Thr Arg Gly Phe Asp Asp Ser Phe Leu Ala Pro His Ser  
180 185 190  
Arg Tyr Ala Asp Phe Pro Ala Ala Leu Ile Arg Asp Tyr Thr Asp Leu  
195 200 205  
Glu Ile Leu Ala Glu Thr Glu Glu Gly Asp Ala Tyr Leu Phe Ala Ser  
210 215 220  
Lys Asp Lys Arg Ile Ala Phe Val Thr Gly His Pro Glu Tyr Asp Ala  
225 230 235 240  
Gln Thr Leu Ala Gln Glu Phe Phe Arg Asp Val Glu Ala Gly Leu Asp  
245 250 255  
Pro Asp Val Pro Tyr Asn Tyr Phe Pro His Asn Asp Pro Gln Asn Thr  
260 265 270  
Pro Arg Ala Ser Trp Arg Ser His Gly Asn Leu Leu Phe Thr Asn Trp  
275 280 285  
Leu Asn Tyr Tyr Val Tyr Gln Ile Thr Pro Tyr Asp Leu Arg His Met  
290 295 300  
Asn Pro Thr Leu Asp  
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<210> 3

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<212> DNA

<213> Artificial Sequence

Corrected sequence listing 11-07

<220>  
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 Oligonucleotide metAfw

<400> 3  
 gatcccatgg ctccttttag tcattcttat 30

<210> 4  
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 <212> DNA  
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<220>  
 <223> Description of Artificial Sequence: Oligonucleotide  
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<400> 4  
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<210> 5  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Oligonucleotide  
 GAPDHfw

<400> 5  
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<210> 6  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Oligonucleotide  
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<400> 6  
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<210> 7  
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 <212> DNA  
 <213> Artificial Sequence

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 <223> Description of Artificial Sequence: Oligonucleotide  
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# Corrected sequence listing 11-07

<212> DNA  
 <213> Artificial Sequence  
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 metArev2  
 <400> 8  
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 <210> 9  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence  
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 <223> Description of Artificial Sequence: Oligonucleotide  
 metAmutfw1; n=1:1:1:1 mixture of A,T,C and G.  
 <400> 9  
 nnncagatca cgccatacga tctac 25  
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 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
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 <223> Description of Artificial Sequence: Oligonucleotide  
 metAmutrev1  
 <400> 10  
 gacgtaatag ttgagccagt tgg 23  
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 <212> DNA  
 <213> Artificial Sequence  
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 <223> Description of Artificial Sequence: Oligonucleotide  
 metAmutfw2; N is a 1:1:1:1: mixture of A, T, C and G  
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 nnnggtttga ttgtaactgg tgcg 24  
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 <212> DNA  
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Corrected sequence listing 11-07

<223> Description of Artificial Sequence: Oligonucleotide  
metAmutrev2

<400> 12

aaagttctga tcctgaatat c

21